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Genomic Selection In Perennial Ryegrass

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IBERS

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Institute of Biological, Environmental and Rural Sciences

Genomic selection in ryegrass

Leif Skjot

PAG XXI January 12-16 2013

defra Department for Environment Food and Rural Affairs

GERMINAL HOLDINGS

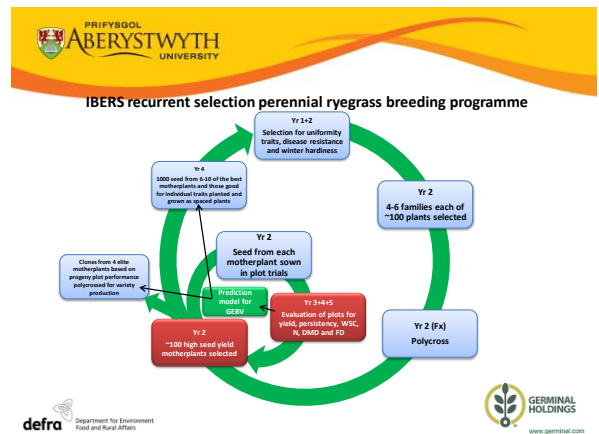
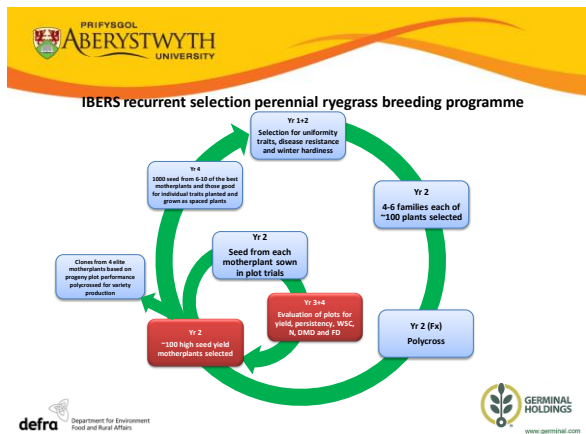
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Recurrent selection in forage crops

Selection and intermating to increase the frequency of desired alleles by repeated cycles

Selection index: $M_j = \sum b_j X_{ij}$

Gupta et al. 2010. Plant Breeding Reviews 33: 145-217



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Genomic selection

Selection decisions based on genomically estimated breeding values derived from determining simultaneous effects of many molecular markers covering the entire genome

Meuwissen et al. (2001) Genetics 157: 1819-1829

Rationale

- Faster selection of candidates for production of synthetics
- Increase the number of recombinations per unit time
- Improve efficiency of introgression of beneficial trait from donor to breeding population?
- Reduce phenotyping costs?

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Genomic selection

Factors affecting accuracy

- **Proximity of marker to locus affecting trait**
Increase marker density improves chances of marker close to QTL (LD = 0.13-0.53 up to 0.2 cM in *L. perenne* breeding population)
- **Size of training population with phenotypes and genotypes**
Increased size likely to increase accuracy
- **Heritability of trait**
Increase replication (costs money)
- **Number of QTL affecting the trait of interest**
Cannot be changed

Genotypes used within the Intermediate diploid population

Parental plants	Generation of introduction
Italian* ecotype (3 plants)	F1
Commercial genotype (2 plants)	F1
RMV resistant genotype (2 plants)	F1
High spring yield genotype (1 plant)	F10
Later heading genotype (1 plant)	F11
Total genotypes so far	9

* Not Italian ryegrass, these are Lolium perenne ecotypes.

Richard Hayes



Heritabilities for various traits

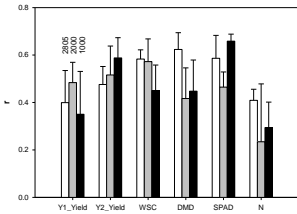
Population	Yield Y1	Yield Y2	WSC	DMD	SPAD	Seed Yield	N
Intermediate	0.38	0.35	0.72	0.66	0.41	0.12	0.40
Late	0.08	0.25	0.56	0.60	0.63	0.10	0.23

Alan Lovatt and Richard Hayes



Cross validation tests in Lolium perenne breeding populations with DArT markers

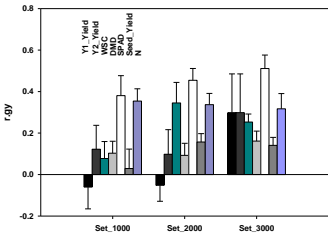
Cross validation in intermediate population at three marker densities



rrBLUP package: Endelman (2011) Plant Genome 4:250-255



Cross validation in late flowering population (105)



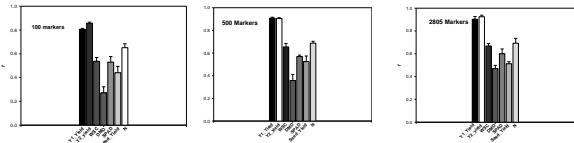
Prediction accuracy with 2805 DArT markers

Training to test population	Yield Y1	Yield Y2	WSC	DMD	SPAD	Seed Yield
Late to Intermediate	0.47	0.34	0.22	0.32	0.01	0.80
Intermediate to late	0.19	0.17	0.22	0.10	0.00	0.00

rrBLUP package: Endelman (2011) Plant Genome 4:250-255

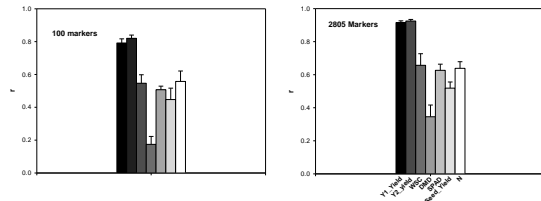


Cross validation combined breeding population (157) Ridge regression





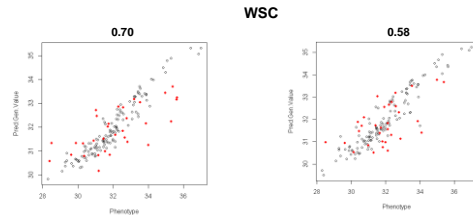
Cross validation in both breeding populations Bayesian LASSO



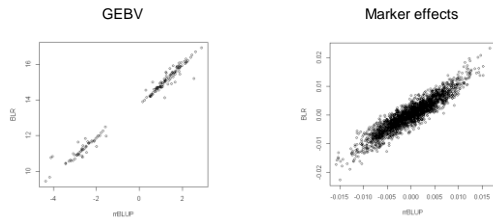
BLR: Perez et al. (2010) Plant Genome 3:106-116



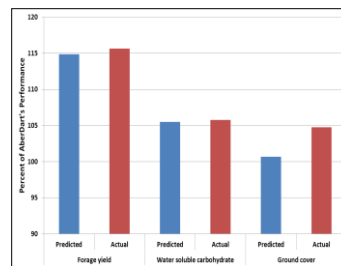
Cross validation in both breeding populations Bayesian LASSO



Genetic values and marker effects Bayesian Lasso vs rrBLUP



Ba14074 Predicted (phenotype) vs. Performance



Clones from 4 elite
motherplants based on progeny
plot performance polycrossed
for variety production

Richard Hayes



Variety development in ryegrass and prediction of best crosses

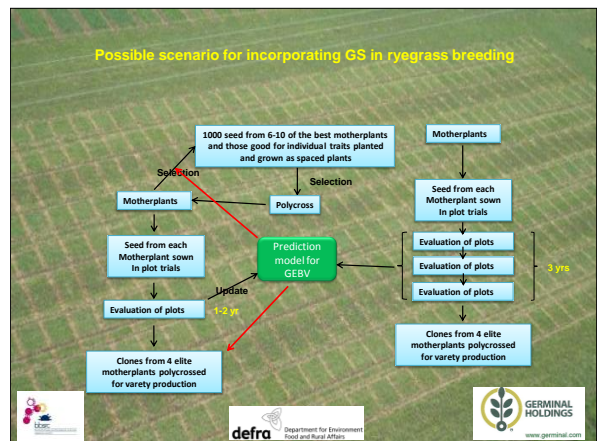
Predicted progeny value

Cross	SPV _{min}	Mean GEBV	SD GEBV
Ba14150 (215, 298, 301, 320)	2.8355	2.5530	0.1555
Random_WSC (39,218,307, 348)	0.2463	-0.0686	0.1749
Ba14281 (High SP42)	5.8445	5.0732	0.4274
Ba14246 (High seed yield)	1.31x10 ⁻⁵	8.48x10 ⁻⁷	
Ba14151 (Seed dr18)	6.2298	1.43x10 ⁻⁵	0.5767
Ba14151 (Seed dr18)	5.6531		

Phenotypic selection vs GEBV

H ²	0.72	0.41	0.12
SPV _{min}	2.8355	2.8355	2.8355
Mean GEBV	2.5530	2.5530	2.5530
SD GEBV	0.1555	0.1555	0.1555
SPV _{min}	0.2463	0.2463	0.2463
Mean GEBV	-0.0686	-0.0686	-0.0686
SD GEBV	0.1749	0.1749	0.1749
SPV _{min}	5.8445	5.8445	5.8445
Mean GEBV	5.0732	5.0732	5.0732
SD GEBV	0.4274	0.4274	0.4274
SPV _{min}	1.31x10 ⁻⁵	1.31x10 ⁻⁵	1.31x10 ⁻⁵
Mean GEBV	8.48x10 ⁻⁷	8.48x10 ⁻⁷	8.48x10 ⁻⁷
SD GEBV			
SPV _{min}	6.2298	6.2298	6.2298
Mean GEBV	1.43x10 ⁻⁵	1.43x10 ⁻⁵	1.43x10 ⁻⁵
SD GEBV	0.5767	0.5767	0.5767
SPV _{min}	5.6531	5.6531	5.6531
Mean GEBV			
SD GEBV			

Zhong and Jannink (2007) Genetics 177: 567-576
Bernardo et al. (2006) Crop Sci 46: 1972-1980





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